

SCORE Search Results Details for Application 10724274 and Search Result us-10-724-274-7.rup.

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This page gives you Search Results detail for the Application 10724274 and Search Result us-10-724-274-7.rup.

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OM protein - protein search, using sw model

Run on: July 19, 2006, 10:36:54 ; Search time 296 Seconds
(without alignments)
340.631 Million cell updates/sec

Title: US-10-724-274-7
Perfect score: 566
Sequence: 1 QIVLTQSPAAMSASLGERVT.....HQYLRSPPTFGGGTKLEIKR 109

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_7.2:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match	Length	DB	ID	Description
1	484	85.5	114	2	Q8K1F1_MOUSE	Q8k1f1 mus musculu
2	469.5	83.0	131	2	Q811C3_MOUSE	Q811c3 mus musculu
3	462	81.6	134	2	Q8VDD0_MOUSE	Q8vdd0 mus musculu
4	459	81.1	106	2	Q2VR04_MOUSE	Q2vr04 mus musculu
5	454	80.2	106	2	Q2VT27_MOUSE	Q2vt27 mus musculu
6	452	79.9	112	2	Q8K1F3_MOUSE	Q8k1f3 mus musculu
7	445	78.6	112	2	Q8K1F2_MOUSE	Q8k1f2 mus musculu

8	441	77.9	106	2	Q2VT29_MOUSE	Q2vt29 mus musculu
9	441	77.9	112	2	Q8K1F0_MOUSE	Q8k1f0 mus musculu
10	441	77.9	235	2	Q58EV6_MOUSE	Q58ev6 mus musculu
11	439	77.6	106	2	Q2VT25_MOUSE	Q2vt25 mus musculu
12	434	76.7	237	2	Q569Y8_MOUSE	Q569y8 mus musculu
13	432	76.3	107	1	KV6F_MOUSE	P04940 mus musculu
14	429	75.8	235	2	Q5XFY8_MOUSE	Q5xfy8 mus musculu
15	427	75.4	107	1	KV6I_MOUSE	P04943 mus musculu
16	426	75.3	107	1	KV6H_MOUSE	P04942 mus musculu
17	426	75.3	237	2	Q3KQK1_MOUSE	Q3kqk1 mus musculu
18	423	74.7	107	1	KV6G_MOUSE	P04941 mus musculu
19	422	74.6	107	1	KV6J_MOUSE	P04944 mus musculu
20	418	73.9	129	1	KV4A_MOUSE	P01680 mus musculu
21	416	73.5	107	1	KV6D_MOUSE	P01678 mus musculu
22	415	73.3	107	1	KV6A_MOUSE	P01675 mus musculu
23	415	73.3	108	1	KV6K_MOUSE	P04945 mus musculu
24	414	73.1	106	2	Q9U410_MOUSE	Q9u410 mus musculu
25	410	72.4	107	1	KV6B_MOUSE	P01676 mus musculu
26	408	72.1	107	1	KV6C_MOUSE	P01677 mus musculu
27	403	71.2	107	1	KV6E_MOUSE	P01679 mus musculu
28	394.5	69.7	236	2	Q6PIH7_HUMAN	Q6pih7 homo sapien
29	388.5	68.6	101	2	Q9JL78_MOUSE	Q9jl78 mus musculu
30	387.5	68.5	97	2	Q9JL76_MOUSE	Q9jl76 mus musculu
31	382	67.5	109	2	Q9UL78_HUMAN	Q9ul78 homo sapien
32	376.5	66.5	108	2	Q9UL79_HUMAN	Q9ul79 homo sapien
33	373	65.9	129	1	KV3L_HUMAN	P18135 homo sapien
34	371.5	65.6	111	1	KV3T_MOUSE	P01672 mus musculu
35	369.5	65.3	108	2	Q9UL77_HUMAN	Q9ul77 homo sapien
36	369	65.2	109	1	KV3F_HUMAN	P01624 homo sapien
37	366.5	64.8	111	1	KV3J_MOUSE	P01662 mus musculu
38	366.5	64.8	111	1	KV3R_MOUSE	P01670 mus musculu
39	366	64.7	107	2	Q96SA9_HUMAN	Q96sa9 homo sapien
40	365.5	64.6	108	2	Q9UL70_HUMAN	Q9ul70 homo sapien
41	365.5	64.6	111	2	Q920E9_MOUSE	Q920e9 mus musculu
42	365.5	64.6	131	1	KV3I_MOUSE	P01661 mus musculu
43	365	64.5	109	2	Q9UL85_HUMAN	Q9ul85 homo sapien
44	365	64.5	129	1	KV3M_HUMAN	P18136 homo sapien
45	364	64.3	109	1	KV3B_HUMAN	P01620 homo sapien

ALIGNMENTS

RESULT 1

Q8K1F1_MOUSE

ID Q8K1F1_MOUSE PRELIMINARY; PRT; 114 AA.

AC Q8K1F1;

DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.

DT 01-OCT-2002, sequence version 1.

DT 07-FEB-2006, entry version 20.

DE Anti-VIPase light chain variable region (Fragment).

GN Name=Gm1418;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muroidea; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=BALB/c; TISSUE=Hyperimmunized spleen;

RA Zhou Y.-X., Taguchi H., Planque S., Karle S., Nishiyama Y., Paul S.;

SCORE Search Results Details for Application 10724274

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OM protein - protein search, using sw model

Run on: July 19, 2006, 10:40:24 ; Search time 39 Seconds
 (without alignments)
 268.914 Million cell updates/sec

Title: US-10-724-274-7
 Perfect score: 566
 Sequence: 1 QIVLTQSPAAMSASLGERVT.....HQYLRSPPTFGGGTKLEIKR 109

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : PIR_80:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES						
Result		Query				
No.	Score	Match	Length	DB	ID	Description
<hr/>						
1	485	85.7	99	2	PH1058	Ig light chain V r
2	484	85.5	130	2	A32513	Ig kappa chain pre
3	479	84.6	99	2	PH1059	Ig light chain V r
4	467	82.5	99	2	PH1060	Ig light chain V r
5	460	81.3	130	2	S04573	Ig kappa chain pre
6	457	80.7	105	2	S26338	Ig kappa chain V r
7	456.5	80.7	108	2	G30560	Ig kappa chain V r
8	456	80.6	113	2	S03410	Ig kappa chain pre

9	455	80.4	107	2	A30562	Ig kappa chain V r
10	455	80.4	140	2	PL0013	Ig kappa chain pre
11	453	80.0	130	2	B32456	Ig kappa chain pre
12	451	79.7	107	2	PC4405	Ig kappa chain V r
13	450	79.5	107	2	B30562	Ig kappa chain V r
14	445	78.6	108	2	PL0278	Ig kappa chain V r
15	441	77.9	108	2	PL0277	Ig kappa chain V r
16	441	77.9	108	2	PL0276	Ig kappa chain V r
17	439	77.6	130	1	JL0079	Ig kappa chain pre
18	437	77.2	106	2	PL0082	Ig kappa chain V r
19	436	77.0	123	2	S05269	Ig kappa chain pre
20	435	76.9	106	2	PS0071	Ig kappa chain V r
21	434	76.7	106	2	B54378	Ig light chain V r
22	434	76.7	109	2	PT0405	Ig light chain V r
23	433.5	76.6	108	2	S38720	Ig light chain V r
24	433	76.5	106	2	G27887	Ig kappa chain V r
25	432	76.3	107	2	PT0406	Ig kappa chain V r
26	431	76.1	104	2	B49049	Ig kappa chain V r
27	430	76.0	103	2	S29591	Ig kappa chain V r
28	429	75.8	107	2	PD0011	Ig kappa chain V r
29	429	75.8	108	2	PS0069	Ig kappa chain V r
30	428	75.6	235	2	S25058	Ig kappa chain - m
31	427	75.4	120	2	S66536	Ig light chain V r
32	426	75.3	96	2	C33730	Ig kappa chain V r
33	425	75.1	109	2	S13699	Ig kappa chain V r
34	425	75.1	124	2	S05267	Ig kappa chain pre
35	424	74.9	108	2	S29581	Ig kappa chain V r
36	423	74.7	107	2	S11119	Ig kappa chain V r
37	422.5	74.6	98	2	PH1061	Ig light chain V r
38	422	74.6	107	2	A42848	Ig light chain V r
39	422	74.6	109	2	PT0404	Ig light chain V r
40	421	74.4	100	2	S29590	Ig kappa chain V r
41	421	74.4	107	2	S11118	Ig kappa chain V r
42	419	74.0	104	2	JC6076	anti-D-dimer monoc
43	419	74.0	106	2	S29583	Ig kappa chain V r
44	418	73.9	129	1	KVMS7B	Ig kappa chain pre
45	415	73.3	107	1	KVMSX4	Ig kappa chain V r

ALIGNMENTS

RESULT 1

PH1058

Ig light chain V region (clone 163.72) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 31-Dec-2004

C;Accession: PH1058

R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

J. Exp. Med. 176, 761-779, 1992

A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cell stimul.

A;Reference number: PH0971; MUID:92381444; PMID:1512540

A;Accession: PH1058

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-99

A;Cross-references: UNIPROT:Q8K1F1; UNIPARC:UPI00001767C0

A;Experimental source: B cell, strain [NZB x NZW]F1

C;Superfamily: immunoglobulin homology

C;Keywords: immunoglobulin

F;16-91/Domain: immunoglobulin homology

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OM protein - protein search, using sw model

Run on: July 19, 2006, 10:45:24 ; Search time 51 Seconds
(without alignments)
187.075 Million cell updates/sec

Title: US-10-724-274-7
Perfect score: 566
Sequence: 1 QIVLTQSPAAMSASLGERVT.....HQYLRSPPTFGGGTKLEIKR 109

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*

1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*

2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*

3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*

4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*

5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*

6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*

7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	SUMMARIES				Description
		Query Match	Length	DB	ID	
1	511	90.3	244	1	US-08-230-843-2	Sequence 2, Appli
2	511	90.3	244	1	US-08-636-936-2	Sequence 2, Appli

3	505	89.2	231	1	US-08-681-432-1	Sequence 1, Appli
4	474	83.7	110	2	US-09-726-219A-256	Sequence 256, App
5	474	83.7	110	2	US-09-196-522-256	Sequence 256, App
6	472	83.4	110	2	US-09-726-219A-237	Sequence 237, App
7	472	83.4	110	2	US-09-196-522-237	Sequence 237, App
8	471	83.2	110	2	US-09-726-219A-257	Sequence 257, App
9	471	83.2	110	2	US-09-196-522-257	Sequence 257, App
10	463	81.8	110	2	US-09-726-219A-254	Sequence 254, App
11	463	81.8	110	2	US-09-196-522-254	Sequence 254, App
12	463	81.8	215	7	5455030-3	Patent No. 5455030
13	460	81.3	108	2	US-08-881-037-74	Sequence 74, Appl
14	459	81.1	129	1	US-08-116-778E-2	Sequence 2, Appli
15	459	81.1	129	1	US-08-438-562-2	Sequence 2, Appli
16	459	81.1	129	1	US-08-483-528B-92	Sequence 92, Appl
17	458	80.9	110	2	US-09-726-219A-255	Sequence 255, App
18	458	80.9	110	2	US-09-196-522-255	Sequence 255, App
19	456.5	80.7	214	2	US-09-653-755A-5	Sequence 5, Appli
20	455	80.4	107	2	US-08-783-853A-11	Sequence 11, Appl
21	455	80.4	107	2	US-09-344-050-11	Sequence 11, Appl
22	455	80.4	112	2	US-08-783-853A-103	Sequence 103, App
23	455	80.4	112	2	US-09-344-050-103	Sequence 103, App
24	453	80.0	108	2	US-09-726-219A-242	Sequence 242, App
25	453	80.0	108	2	US-09-196-522-242	Sequence 242, App
26	453	80.0	235	2	US-09-238-741-2	Sequence 2, Appli
27	452	79.9	128	1	US-08-476-275-4	Sequence 4, Appli
28	452	79.9	128	2	US-08-475-815B-7	Sequence 7, Appli
29	452	79.9	128	2	US-08-475-813-4	Sequence 4, Appli
30	451	79.7	129	1	US-08-449-287-2	Sequence 2, Appli
31	451	79.7	235	2	US-09-423-439-18	Sequence 18, Appl
32	451	79.7	235	2	US-09-423-439-58	Sequence 58, Appl
33	451	79.7	235	2	US-09-011-769A-23	Sequence 23, Appl
34	451	79.7	248	7	5455030-11	Patent No. 5455030
35	450	79.5	106	1	US-07-634-278-1	Sequence 1, Appli
36	450	79.5	106	1	US-07-634-278-16	Sequence 16, Appl
37	450	79.5	106	1	US-08-477-728-1	Sequence 1, Appli
38	450	79.5	106	1	US-08-477-728-16	Sequence 16, Appl
39	450	79.5	106	1	US-08-474-040-1	Sequence 1, Appli
40	450	79.5	106	1	US-08-474-040-16	Sequence 16, Appl
41	450	79.5	106	1	US-08-487-200-1	Sequence 1, Appli
42	450	79.5	106	1	US-08-487-200-16	Sequence 16, Appl
43	450	79.5	106	1	US-08-488-113B-163	Sequence 163, App
44	450	79.5	106	1	US-08-477-484B-163	Sequence 163, App
45	450	79.5	106	1	US-08-107-669D-49	Sequence 49, Appl

ALIGNMENTS

RESULT 1

US-08-230-843-2

; Sequence 2, Application US/08230843

; Patent No. 5582826

; GENERAL INFORMATION:

; APPLICANT: SHIMAMURA, TOSHIRO

; APPLICANT: HAMURO, JUNJI

; APPLICANT: NAKAZAWA, HARUMI

; APPLICANT: KANAYAMA, YUKA

; APPLICANT: SUGAMURA, KAZUO

; APPLICANT: TAKESHITA, TOSHIKAZU

; TITLE OF INVENTION: IMMUNOSUPPRESSANT

; NUMBER OF SEQUENCES: 12

SCORE Search Results Details for Application 10724274 and Search Result us-10-724-274-7.rag.

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OM protein - protein search, using sw model

Run on: July 19, 2006, 10:36:24 ; Search time 198 Seconds
(without alignments)
251.700 Million cell updates/sec

Title: US-10-724-274-7
Perfect score: 566
Sequence: 1 QIVLTQSPAAMSASLGERTV.....HQYLRSPPTFGGGTKLEIKR 109

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_8:
1: geneseqp1980s:
2: geneseqp1990s:
3: geneseqp2000s:
4: geneseqp2001s:
5: geneseqp2002s:
6: geneseqp2003as:
7: geneseqp2003bs:
8: geneseqp2004s:
9: geneseqp2005s:
10: geneseqp2006s:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query				
No.	Score	Match	Length	DB	ID
					Description

1	566	100.0	109	8	ADT77625	Adt77625 IIIA1 VL p
2	566	100.0	109	9	AEB51144	Aeb51144 Mouse ant
3	566	100.0	215	8	ADQ31885	Adq31885 Antibody
4	566	100.0	215	8	ADT77644	Adt77644 Antibody
5	566	100.0	215	9	AEB51163	Aeb51163 Chimeric
6	566	100.0	215	10	AEF12091	Aef12091 Anti-alph
7	566	100.0	215	10	AEF16423	Aef16423 Chimeric
8	564	99.6	215	8	ADT51708	Adt51708 M200 anti
9	561	99.1	130	8	ADQ31877	Adq31877 Antibody
10	561	99.1	130	8	ADQ31866	Adq31866 Murine an
11	561	99.1	130	8	ADQ31881	Adq31881 Antibody
12	561	99.1	130	8	ADT77640	Adt77640 Antibody
13	561	99.1	130	8	ADT77636	Adt77636 Antibody
14	561	99.1	130	9	AEB51155	Aeb51155 Chimeric
15	561	99.1	130	9	AEB51159	Aeb51159 Chimeric
16	561	99.1	130	9	AED49296	Aed49296 Anti-alph
17	561	99.1	130	9	AED49292	Aed49292 Anti-alph
18	534	94.3	110	8	ADT75068	Adt75068 Light cha
19	534	94.3	110	8	ADT75050	Adt75050 Light cha
20	533	94.2	109	10	AEF24398	Aef24398 Mouse mat
21	533	94.2	131	9	ADW14710	Adw14710 Monoclonal
22	533	94.2	131	10	AEF24378	Aef24378 Mouse PAN
23	524	92.6	110	9	AED34781	Aed34781 Chimeric
24	524	92.6	216	9	AED34778	Aed34778 Chimeric
25	522	92.2	131	9	ADW14791	Adw14791 Anti-KIR
26	521	92.0	110	9	ADW86132	Adw86132 Novel cyt
27	520	91.9	215	8	ADN97547	Adn97547 Artificia
28	520	91.9	483	8	ADN97549	Adn97549 Artificia
29	519	91.7	110	8	ADT75126	Adt75126 Light cha
30	518	91.5	108	3	AAB10021	Aab10021 H. pylori
31	518	91.5	110	8	ADT75052	Adt75052 Light cha
32	518	91.5	129	8	ADS94357	Ads94357 Antibody
33	517	91.3	108	8	ADT89037	Adt89037 Murine pl
34	517	91.3	113	10	AEG03168	Aeg03168 CD200 ant
35	512	90.5	108	3	AAV53591	Aav53591 Light cha
36	512	90.5	111	8	ADT75069	Adt75069 Light cha
37	511	90.3	111	8	ADT75060	Adt75060 Light cha
38	511	90.3	244	2	AAR60780	Aar60780 Fv(GP-2)
39	510	90.1	106	10	AEF02311	Aef02311 Mouse mon
40	510	90.1	109	9	AEA17138	Aea17138 Human TNF
41	509	89.9	112	6	ABJ19266	Abj19266 Anti-huma
42	509	89.9	282	6	ABJ19276	Abj19276 Anti-huma
43	507	89.6	109	8	ADQ31867	Adq31867 Humanised
44	507	89.6	109	8	ADT77626	Adt77626 1 VL pept
45	507	89.6	109	9	AEB51145	Aeb51145 Humanized

ALIGNMENTS

RESULT 1

ADT77625

ID ADT77625 standard; peptide; 109 AA.

XX

AC ADT77625;

XX

DT 13-JAN-2005 (first entry)

XX

DE IIIA1 VL peptide.

XX